

Figures

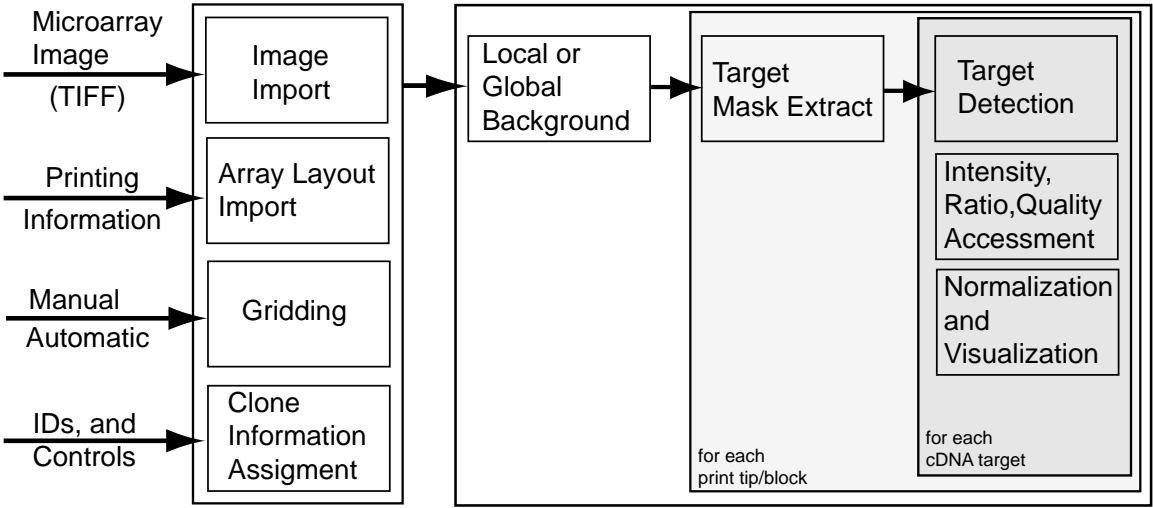


Figure 1. Image analysis block diagram.

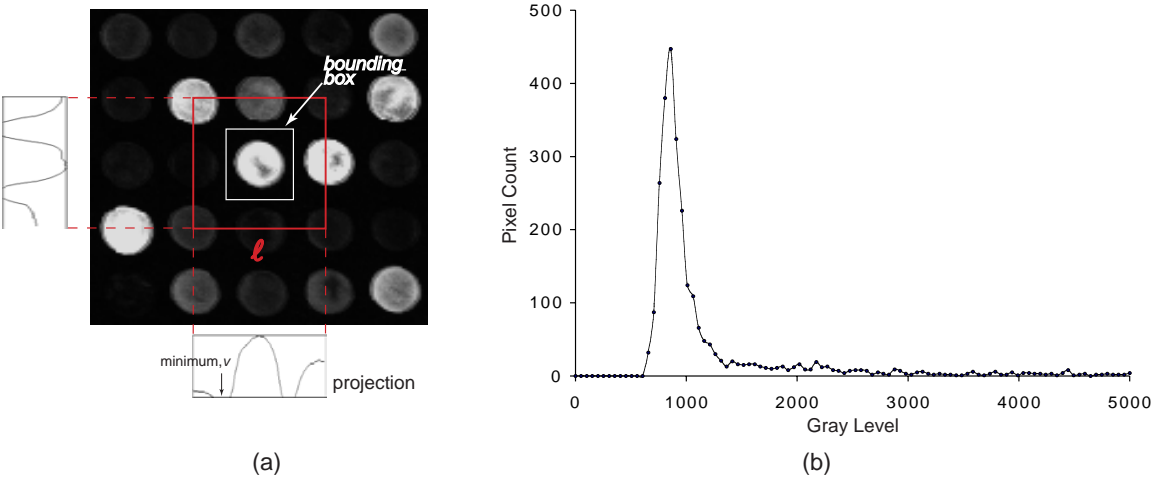


Figure 2. Background extraction.

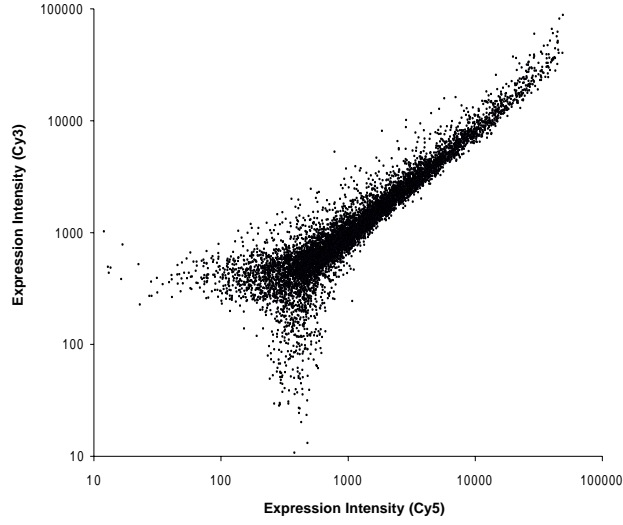


Figure 3. The expression intensity scatter plot. Each spot represents a gene with expression intensities from two cell-types.

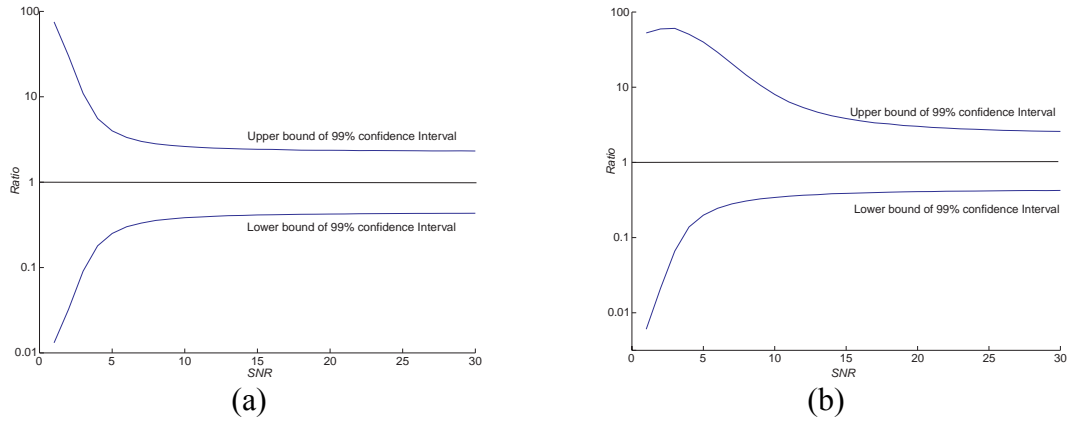


Figure 4. (a) The 99% confidence interval for for $c = 0.2$, $b = 1000$, and $\alpha = 0.10$, or $T = [N(100s, 20s) + N(0, 100)] / [N(100s, 20s) + N(0, 100)]$. The average of 10 simulations is reported here, and each simulation was performed by 10^5 data points for each s value. (b) An exact same setting except for the background level such that $b_G = 3b_R = 3000$.

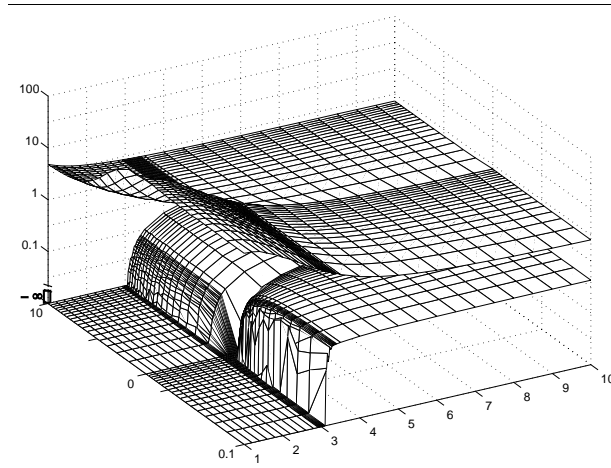


Figure 5. Confidence intervals with different background variation for both channels. The cv for the ideal condition is 0.20.

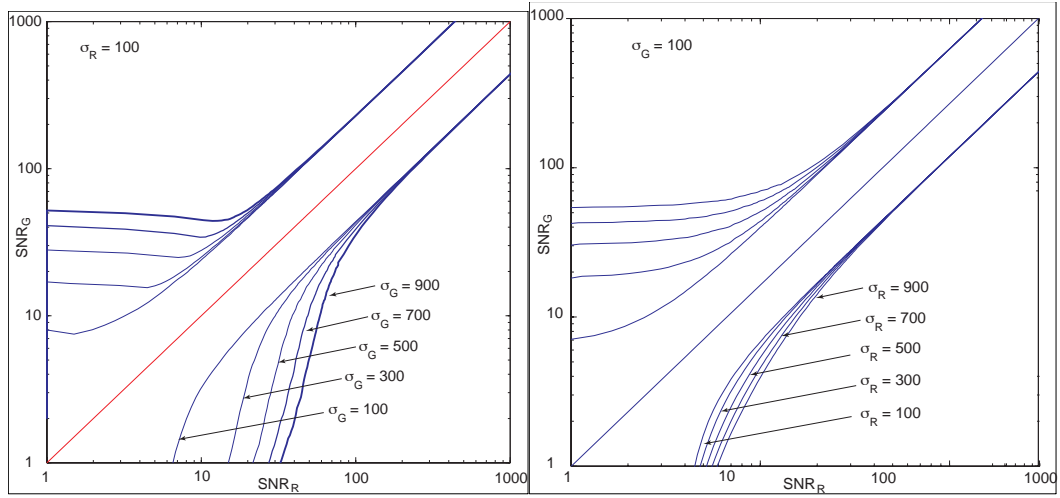


Figure 6. Confidence intervals derived from the null hypothesis estimate $p_k = (R_k + G_k)/2$.

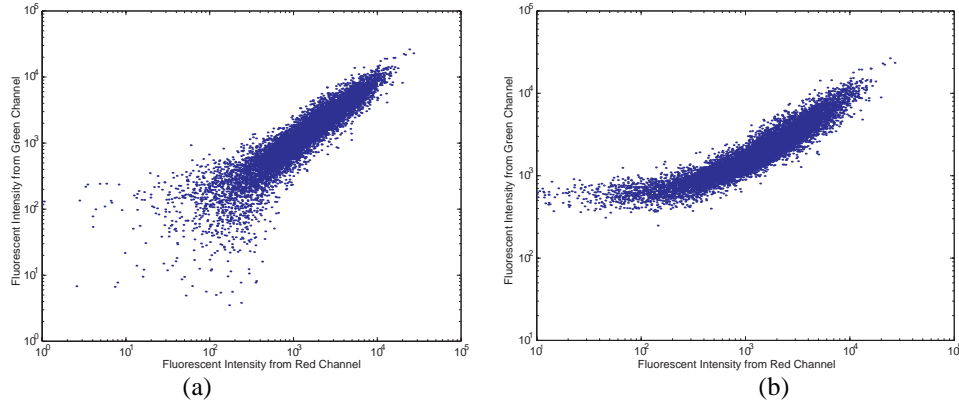


Figure 7. Scatter plot of simulated expression data. The expression intensity is simulated by an exponential distribution with mean of 2000. The intensity measurement for each channel is further simulated by using a normal distribution with mean intensity from the exponential distribution and a constant cv of 0.2. (a) 10,000 data points with no bias from background estimation. (b) 10,000 data points with background estimation bias of 500.

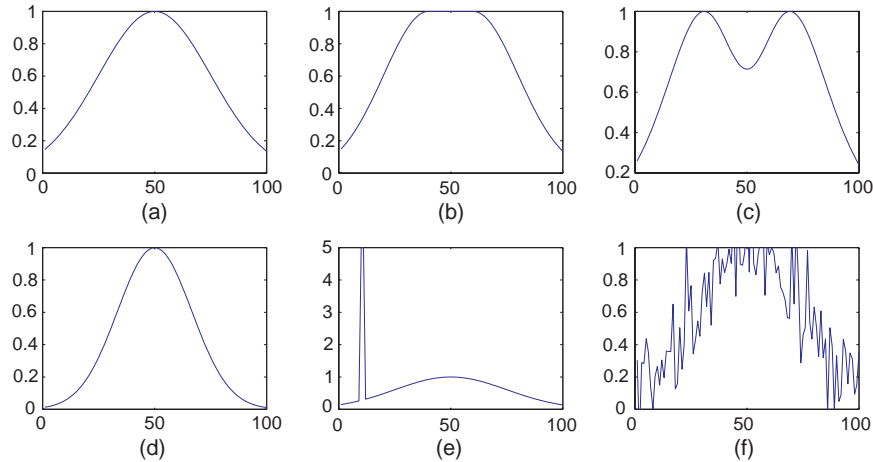


Figure 8. Typical target shape in 1-D. Total of 100 sample points. (a) Gaussian-shape. Created with normalized $N(50, 25)$. $cv = 0.48$. (b) Flat-top shape. Created by normalized $N(50, 20)$ on both side. Middle 20 samples are set to 1.0. $cv = 0.45$. (c) Donut-shape. Created by normalized $N(50, 25)$ subtracted by $0.6 \times (\text{normalized } N(50, 10))$. $cv = 0.31$. (d) Steep-rising bell-shape. Created by $N(50, 17)$. $cv = 0.81$. (e) Same as (a) except samples 10 and 11 which are set to 5. $cv = 0.91$. And (f) Same as (a) but some noise are added. $cv = 0.59$.

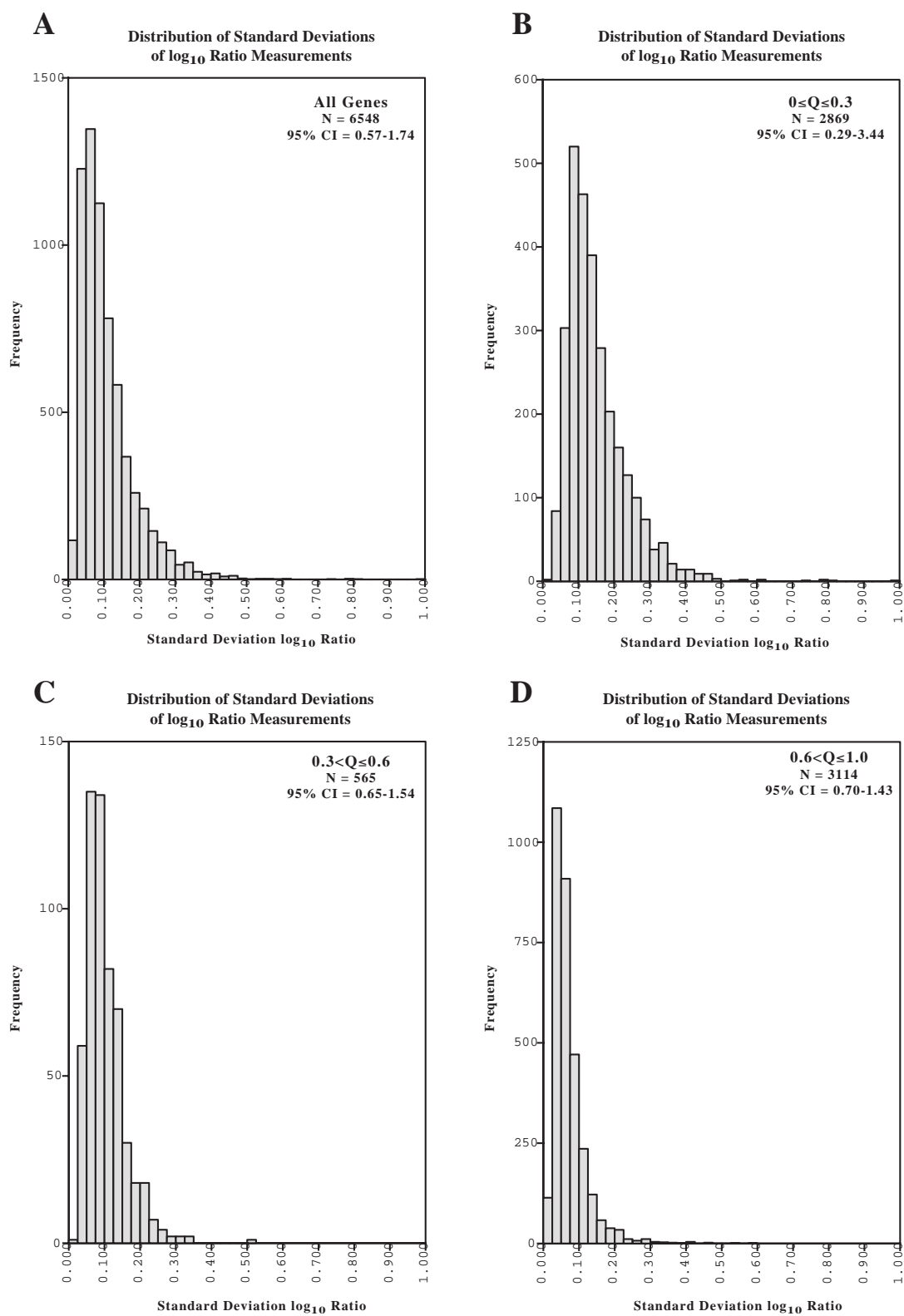


Figure 9. Histograms of the standard deviations of the \log_{10} ratio values for all genes from 8 replicated experiments.